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OM protein - protein search, using sw
                                                        Copyright
                                                          GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
  mode1
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Run on: March 7, 2005, 07:04:17; Search time 8.94985 Seconds (without alignments) (without alignments)
1193.323 Million cell updates/sec

Title: Perfect score: US-09-939-537-37 591

Sequence: 1 TRFSRSAEPPAYQQGQNQLY.....LSTATKDTYDALHMQALPPR 111

Scoring table: 283416 seqs, Gapop 10.0 , 96216763 residues Gapext 0.5

BLOSUM62

283416

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0
seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:* 1: pir1:* pir2:* pir3:* pir4:*

Database

and is Pred. No. No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

Result

	27		69	69	69	. 22				18 70	71	73	15 73.	14 73	13 73			10 76		. 80	378	6 378.	5 389	4 471.	3 471.	2 476.	1 58	Result No. Score
лω	69 11.7	9	11	.5 11.8	.5 11.8	_	_	11.	70 11.8	.5 11.9		.5 12.4	.5 12.4	•	.5 12.4			12.	13.	14.	u	5 64	39 65.8	5 79	5 79	.5 80.6	33 98.6	Query
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conserved hypothet ATP-dependent DNA	hypothe	വ	m		_	erythrocyte membra			hypothetical prote	protein T1N15.25 [hypothetical prote	nuclear protein SA	conserved hypothet	7	general stress pro	CREB-binding prote	probable late embr	probable ATP-depen		regulator protein	T-cell receptor CD	T-cell receptor io	T-cell receptor CD	T-cell surface gly	T-cell receptor ze	T-cell receptor CD	1 receptor	Description

A40104
T-cell receptor CD3 zeta chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004

C;Accession: A40104; I55293 R;Weissman, A.M.; Baniyash, M.; Hou, D.; Samelson, L.E.; Burgess, W.H.; Klausner, Science 239, 1018-1021, 1988
A;Title: Molecular cloning of the zeta chain of the T cell antigen receptor.
A;Reference number: A40104; MUID:88145643; PMID:3278377
A;Accession: A40104

R.D.

A;Cross-references: UNIPROT:P24161; GB:M19729; NID:g201131; PIDN:AAA40171.1; PID:g201132 R;Baniyash, M.; Hsu, V.W.; Seldin, M.F.; Klausner, R.D. J. Biol. Chem. 264, 13252-13257, 1989 A;Title: The isolation and characterization of the murine T cell antigen receptor zeta classification.

Ü

A; Molecule type: mRNA A; Residues: 1-164 <WEI>

A;Status: preliminary

A;Reference number: I55293; MUID:89327299; PMID:2787796 A;Accession: I55293

preliminary; translated from GB/EMBL/DDBJ

12.1	4 43	41 42	40	9	38	37	36	35	3. <u>4</u>	ω W	32	31	30
67	67	67 67	67.5	67.5	67.5	67.5	67.5	67.5	67.5	68	68	68	68
11.3	11.3	11.3	11.4	11.4	11.4	11.4	11.4	11.4	11.4	11.5	11.5	11.5	11.5
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ALIGNMENTS

C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: A31768
R;Weissman, A.M.; Hou, D.; Orloff, D.G.; Modi, W.S.; Seuanez, H.; O'Brien, S.J.; Klausnes
Proc. Natl. Acad. Sci. U.S.A. 85, 9709-9713, 1988
A;Tile: Molecular cloning and chromosomal localization of the human T-cell receptor zeta
A;Reference number: A31768; MUID:89071765; PMID:2974162 ð 문 A;Cross-references: UNIPROT:P20963; GB:J04132; NID:g623041; PIDN:AAA60394.1; PID:g623042 C;Keywords: phosphoprotein; T-cell receptor; transmembrane protein F;1-21/Domain: signal sequence #status predicted <SIG> F;22-163/Product: T-cell receptor zeta chain #status predicted <MAT> A;Accession: A31768 A;Molecule type: mRNA A;Residues: 1-163 <WEI> A31768
T-cell receptor zeta chain precursor - human 밁 S Query Match Best Local Similarity Matches 109; 114 OKDKWABAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR 163 62 QXDKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR 111 54 KFSRSAEPPAYOOGONOLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL 2 RFSRSAEPPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNEL 98.6%; ilarity 99.1%; Conservative 1; Mismatches Score 583; DB 2; Pred. No. 1.9e-49; .. Length 163; Indels 0, Gaps 113 61 0

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T-cell surface glycoprotein CD3 zeta chain - sheep (5) species: Ovis orientalis aries, Ovis ammon aries (domest C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_c;Accession: 146424, S22980 R;Hein, W.R.; Tunnacliffe, A.
Immunogenetics 37, 279-284, 1993 A;Title: Invariant components of the sheep T-cell antigen A;Reference number: 146424; MUID:93131305; PMID:8420837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell receptor zeta chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 05-Nov-1999
C;Accession: JC4664
R;Hagens, G.; Galley, Y.; Glaser, I.; Davis, W.C.; Baldwin, C.L.; Clevers, H.; Dobbelaer
Gene 169, 165-171, 1996
A;Title: Cloning, sequencing and expression of the bovine CD3 epsilon and TCR-zeta chain
A;Reference number: JC4663; MUID:96194796; PMID:8647441
                                                                            A;Accession: 146424
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-166 <HEI>
A;Cross-references: UNIPROT:P29329; EMBL:Z12968; NID:g1399; PIDN:CAA78312.1; PID:g1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: tcr-zeta
C;Keywords: GTP binding; signal transduction;
F;129-146/Region: GDP/GTP-binding
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A; Residues: 1-166 < HAQ2
A; Cross-references: GB:UZ5688; NID:g1263011; PIDN:AAC48548.1; PID:g1263012
C; Comment: This protein plays a pivotal role in linking T-cell receptor-trymphokine receptor gene expression.
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C;Keywords: phosphoprotein; T-cell receptor; transmembrane protein
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C;Genetics:
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  Query Match
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                                                                words: glycoprotein
  Local Similarity
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Local Similarity 81.4%;
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Pred. No. 1.3e-38;
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Pred. No. 4.2e-39;
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No. 1.3e-38;
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#text_change 09-Jul-2004
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                    Length 166;
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A;Cross-references: GB:S51932; NID:g261998; PIDN:AAB24559.1; PID:g261999
A;Experimental source: thymus
A;Note: sequence extractef from NCBI backbone (NCBIP:120865)
R;Lerner, A.; Diener, A.C.; Reinherz, E.L.; Clayton, L.K.
Eur. J. Immunol. 22, 2135-2140, 1992
A;Title: Human genomic sequences corresponding to murine CD3eta-related transcripts: A;Accession: I49587; MUID:92347411; PMID:1322304
A;Accession: I49587
A;Status: translated from GB/EMBL/DDBJ
A;Rosidues: 1-188 <-RES>
A;Cross-references: GB:L03353; NID:g192508; PIDN:AAA37401.1; PID:g192509
C;Keywords: T-cell receptor
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S54817
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A;Title: Differential regulation of T-cell receptor processing and surface expression A;Reference number: A45089; MUID:93100325; PMID:1464613
A;Accession: A45089
                                                                       A;Molecule type: mRNA
A;Residues: 1-177 <NOC>
A;Cross-references: EMBI
C;Keywords: T-cell recep
                                                                                                                                                                                                           R;Nocentini, G.; Ronchetti, S.; Bartoli, A.; Testa, G.; d'Adamio, submitted to the EMBL Data Library, January 1995
A;Description: T cell receptor iota: an alternatively spliced pro
                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 08-Jul-1995 #sequence_revision
C;Accession: S54817
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A45089
C. Species: Mus musculus (house mouse)
C. Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C. Accession: A45089; I49587
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A;Reference number: S54817
A;Accession: S54817
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               64.0%;
82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
 5;
                                                                                             NID: g809045; PIDN: CAA59015.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 389; DB 2;
Pred. No. 1.5e-30;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                             mouse
Score 378.5; DB 2
Pred. No. 1.5e-29;
5; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                       21-Jul-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                           142
                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 188;
                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                               product
                                                                                               PID:g809046
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Gaps
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                                                                                                                                                                                                               of the T cell recep
                                                                                                                                                                                                                                                   Riccardi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
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regulator protein white collar 1 - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 15-Mar-2004
C;Accession: S69206
R;Ballario, P.; Vittorioso, P.; Magrelli, A.; Talora, C.; Cabibbo, A.; Macin
EMBO J. 15, 1650-1657, 1996
A;Title: White collar-1, a central regulator of blue light responses in Neur
A;Reference number: S69206, MUID:96203083; PMID:8612589
A;Accession: S69206
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <BAL>
A;Cross-references: EMBL:X94300; NID:g1279576; PID:g1480115
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Int. Immunol. 2, 1117-1119, 1990

A;Title: CD3zeta and eta chains are produced by alternative splicing fr A;Reference number: A60374; MUID:91190781; PMID:2150596

A;Accession: A60374

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 144-206 < COHN>
R;Jensen, J.P.; Cenciarelli, C.; Hou, D.; Rellahan, B.L.; Dean, M.; Wei

J. Immunol. 150, 122-130, 1993

A;Reference number: A46522; MUID:93107707; PMID:8417118

A;Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T-cell receptor CD3 eta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Oct-1990 #seguence_revision 23-Oct-1990 #text_change 09-Jul-2004
C;Accession: A35900; A60374; G46522
R,Jin, Y.J.; Clayton, L.K.; Howard, F.D.; Koyasu, S.; Sieh, M.; Steinbrich, R.; Tarr, G. Proc. Natl. Acad. Sci. U.S.A. 87, 3319-3323, 1990
A;Title: Molecular cloning of the CD3eta subunit identifies a CD3zeta-related product in A;Reference number: A35900; MUID:90239005; PMID:2139725
A;Accession: A35900
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 멍
                             A; Introns: 967/3
C; Keywords: zinc:
F; 932-991/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S
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A; Residues: 1-206 <JIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no acids,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RFSRSAEPPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGK-PRRKNPQEGLYNE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 64.0%;
Similarity 82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOKUKMAEAYSEIGMKGERRRGKGHDGLYQ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQKDKMAEAYSEIGTKGERRRGKGHDGLYQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQKDKWAEAYSEIGMKGERRRGKGHDGLYQ 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSRSAEPPAYQQQQNQLYNELNLGRREEYDVLDKRRGRDPEMGGK-PRRKNPQEGLYNE
finger
: GATA-type zinc finger homology <GZF>
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                                                                                                                                                                                                                                                                                                                                          A.; Macino,
                                                                                                                                                                                                                                                                                      in Neurospora,
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hypothetical protein F18H3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21095
R;Coles, L.
                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                           A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein
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A;Experimental source: clone F18H3
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A; Residues: 1-692 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A; Accession: T21095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
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Best Local
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                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                            486
                                                                                                                                                       543 VQMGGAPIRQQGPAPRGAPQKPFYQGPPRQQQPQQHSQQPAQQPGQQGQGQSGIVIHGQE
                                                                                                                                                                                          3
                                                                                                                   94 TATKDTYDALHM--QALP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 PQEGLYNELQKDKMAEAYSE----IGMKGERRRGKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                             9 PPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDP------
                                                                                                                                                                                                                                                                                               30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNDG-FSDYQLDNMSGNYGDMTGGMGMSGHSSPYAGQNIMAMSDHSGGYSHMSPNVMGNM 189
                                                                                                                                                                                        -EMGGKPRRN-----POEGLYNELOKDKMAEAYSEIGMKGERRRGKGHDGL-YQGLS
                                                                                                                                                                                                                          PPGQRVFQNQMFMQYPFNQRQVY---PQQQGRPPMRTNDGRPQYGMAPRPAGAPRVGGPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPTTNQGNSTIHASDVTMSGGSDSLDEIIQQNLDEMHRRRSVPQPYGGQTRRLSMFDYAN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPAYQQGQNQLY-----NELNLGRREEYDVLDKRRGRDPEMGGKPRR-----KN
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y 21.7%; Pred. No. v,
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24.8%; Pred. No.
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                                                                                    614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                 DB 2;
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(Drosophila melanogaster)
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probable ATP-dependent RNA helicase Dbp45A - fruit fly (Drosophila melanoga N;Alternate names: DEAD-box protein C;Species: Drosophila melanogaster C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004 C;Accession: S38329; S39749
R;Lavoie, C.A.; Harvey, M.; Lasko, P.F.

R;Lavoie, C.A.; Harvey, M.; Lasko, P.F. Biochim. Biophys. Acta 1216, 140-144, 1993 A;Title: DBp45A encodes a Drospphila DBAD box protein with similarity A;Reference number: S38329; MUID:94032476; PMID:7692973

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putative yeast

A;Accession: S38329 A;Molecule type: DNA A;Residues: 1-527 <LAV1>

A;Cross-references: UNIPROT:Q07886; GB:L13612
A;Note: the authors translated the codon TGC for residue 211 as Ser, G
4 as Gln, GGT for residue 225 as Arg, GTG for residue 228 as Leu, TCG 212 9 as

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A;Gene: Dbp45A
A;Cross-references: FlyBase:FBgn0010220
A;Cross-references: FlyBase:FBgn0010220
A;Introns: 26/1; 206/3; 262/2; 382/1; 433/2
C;Keywords: ATP; nucleotide binding; P-loop
F;51-58/Region: nucleotide-binding motif A (F
F;153-158/Region: nucleotide-binding motif B
F;157-160/Region: DEAD motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lavoie, C.A.; Harvey
submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Rebidues: 1-326,'I',328-406,'C',408-492,'Y',494-527 <LAV2>
A;Rebidues: 1-326,'I',328-406,'C',408-492,'Y',494-527 <LAV2>
A;Cross-references: EMBL:H13612; NID:g304670; PIDN:AAA16339.1; PID:g304671
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable late embryogenesis abundant protein - carrot (fragment)
N,Alternate names: LEA protein
C;Species: Daucus carota (carrot)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S39749
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T14305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lin, X.; Hwang, G.J.; Zimmerman, J.L. submitted to the EMBL Data Library, January 1996 A, Description: Isolation and characterization of a diverse set of A;Reference number: Z17968 A;Accession: T14305
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A; Residues: 1-136 <LIN>
             C; Accession: T13828
R; Akimaru, H.; Chen,
Nature 386, 735-738,
                                                 CREB-binding protein homolog - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13828
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Best Local 9
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:Q39681; EMBL:U47096; NID:g1276968; PID:g1276969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430
Drosophila CBP is a co-activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRKNPQEGLYNELQKDKMAE------AYSEIG---MKGER------RRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGR-----SRATQE 492
                                                                                                                                                                                                                                                                                                                   EEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQ-----KDKWAEAYSEIGMKGERRRG
                                                                                                                                                                                                                                                                                 KGHDGLYQGLSTATKDTYDALH 104
                                                                                                                                                                                                           KAKDKAYETAESAKKKANEAYY 80
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ilarity 23.5%;
Conservative 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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                     Y.; Dai, P.; Hou, D.X.; Nonaka, M.; Smolik, 1997
                                                                                                                                                                                                                                                                                                                                                                               12.5%;
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                                                                                                                                                                                                                                                                                                                                                             14;
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                                                                                                                                                                                                                                                                                                                                                                                 Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                               core 74; DB 2; red. No. 3.7; Mismatches 38
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                                               S.M.; Armstrong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes from carrot some
           in hedgehog
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J. Hacteriol. 174, 4361-4373, 1992
A;Title: Transcriptional regulation of Bacillus subtilis glucose starvation-inducible ger A;Title: Transcriptional regulation of Bacillus subtilis glucose starvation-inducible ger A;Title: Transcriptional regulation of Bacillus subtilis glucose starvation-inducible ger A;Title: Transcriptional regulation of Bacillus subtilis glucose starvation-inducible ger A;Reference number: S26183
A;Reference number: S26183
A;Roclecule type: DNA
A;Residues: 1-123 -MUE>
A;Roclecule type: DNA
A;Residues: 1-123 -MUE>
A;Roclecule type: DNA
A;Residues: 1-123 -MUE>
A;Cross-reference: UNIPROT:P26907; EMBL:X56680; NID:g39933; PIDN:CAA40009.1; PID:g39934
A;Cross-reference: UNIPROT:P26907; EMBL:X56680; NI, Fullia, X.; Ful
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A;Accession: T13828
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-3190 < AKI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Bacillus subtilis
C;Date: 22-Nov-1993 #sequence revision 02-Jun-1994
C;Dates 22-Nov-1993 #sequence revision 02-Jun-1994
C;Accession: S26183; H69637; S21381
C;Accession: S26183; H69637; S21381
R;Mueller, J.P.; Bukusoglu, G.; Sonenshein, A.L.
J. Bacteriol. 174, 4361-4373, 1992
J. Bacteriol. 174, 4361-4373, 1992
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                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Z99106; GB:AL009126; NID:g2632653; PIDN:CAB12247.1; PID:g2632740
A;Experimental source: strain 168
C;Comment: This protein of unknown function is induced by glucose starvation or phosphat
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-123 < KUN>
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                                                                                                                                                            F;13-117/Region:
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Best Local (
           Query Match
Best Local S
Matches 22
                                                                                                                                                                                      Superfamily: gsiB protein Keywords: tandem repeat
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y match 12.4%;
Local Similarity 31.4%;
hes 22; Conservative
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                                                                                                                                                        20-residue repeats (G-X-K-G-G-E-A-T-S-K-N-H-D-K-E-F-Y-Q-E-I)
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                                                       Score 73.5;
Pred. No. 3.
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                                                                                                    DB 1;
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                                                                                                Length 123;
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Mismatches

28;

Gaps

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RESULT 15
H70415
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A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: Ap0317
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-360 <KUR>
A;Cross-references: UNIPROT:Q8ZDG6; GB:AL590842; PIDN:CAC92845.1; PID:g15980589; GSPDB:C;Genetics:
A;Gene: rlpA
C;Superfamily: rplA lipoprotein
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                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-374 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: H70415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein aq_1336 - Aquifex aeolicus C;Species: Aquifex aeolicus C;Capecies: Aquifex aeolicus C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004 C;Accession: H70415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
AF0317
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                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.; O
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Best Local Similarity
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                                                                                                                  19 LYNELNLGR-REEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK--DKMAEAYSEIGM 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 QKDKMAEAYSEIGMK----GERRRGKGHDGLYQGLSTATKDTYDALHMQALPP 110
76 KGERRRGKGHDGLYQGLSTATKDT-YDAL 103
                                                                           81 LYNERFLNKLKEEREKILKKGYREPSHAGQAYPENPQE-LKNFIEETVNKNSEKFKARGI 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 OPPAPOQQVQQTYSGPVEEIG-GAEPRYEPFNPNVNQDYKVNGQSYRIIKDPQN-----
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                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.4%; Score 73.5; Ilarity 25.9%; Pred. No. 12; Conservative 17; Mismatches
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29.2%; Pred. No. 13;
tive 21; Mismatches
                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                           37; Indels
                                                                                                                                                                                                                          Length 374;
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